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Echinodermata is one of the biggest phyla containing 5 classes (Sea cucumber, Sea urchin, Sea star, Brittle star and Sea lily), and found at all ocean depths and all latitudes. This group is a member of deuterostomes which is closely related to chordates, so it has been used for the embryology from the past. However on fisheries, it is very minor group in the world except Asian countries, so there is little genetic information for resource management at present. In our laboratory, we have been trying to make the basis of the population genetic study of echinoderms from the development of DNA markers. Here I introduce the three outcomes in our lab. about three echinoderm groups, a sea cucumber, a sea urchin, and two sea stars.

Japanese sea cucumber, *Apostichopus japonicus*, is the almost only one marketed species in Japan, and also popular fishery species in China, Korea and Russia. This species has three color variants, namely Red, Green and Black, however the taxonomic relationship among them has not long been clear because of few morphological traits of it. So we tried to evaluate the color trait quantitatively, and then investigated the genetic differentiation among them using allozyme and microsatellite DNA markers. As results, Red was clearly divided from the other color types, both in color trait and in genetic analysis showing the reproductive isolation of it. On the other hand, Green and Black showed continuous color distribution and no genetic difference suggesting the genetic homogeneity of them.

Strongylocentrotus nudus is a common sea urchin distributed around Japan. In order to detect the management units of it, we carried out mtDNA sequence analysis for the samples from 5 localities. As results, the typical haplotype networks suggesting the recent population explosion of the species were observed, and genetic compositions showed no statistic difference among the localities. Therefore, the present genetic structure which shows lack of genetic difference among the localities is thought to be strongly influenced by their recent historical expansion, and it is difficult to discuss about the present gene flow among the localities.

Asterina pectinifera and *Asterias amurensis* are common sea stars distributed along the coastal side of Japan. They have very similar life history but different taxonomic back ground. From the allozyme and mtDNA PCR-RFLP analysis, very contractive genetic structure was detected between them, which is genetic uniformity of *Asterina pectinifera*, and highly divergent genetic structure of *Asterias amurensis*. The difference in population structure of the two species was thought to be caused by the length of the history of the populations.

Through the introduction of the three studies, here I arrange the characteristics of the DNA markers on stock identification, and suggest the future subject for genetic management of echinoderms.